

	20		25		30										
Ala	Ala	Pro	Thr	Thr	Gly	Val	Val	Pro	Ala	Ala	Ala	Asp	Glu	Val	Ser
	35					40						45			
Ala	Leu	Thr	Ala	Ala	Gln	Phe	Ala	Ala	His	Ala	Gln	Met	Tyr	Gln	Thr
	50				55							60			
Val	Ser	Ala	Gln	Ala	Ala	Ala	Ile	His	Glu	Met	Phe	Val	Asn	Thr	Leu
	65				70					75			80		
Val	Ala	Ser	Ser	Gly	Ser	Tyr	Ala	Ala	Thr	Glu	Ala	Ala	Asn	Ala	Ala
			85						90				95		
Ala	Ala	Gly													

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Met	Ser	Phe	Val	Thr	Thr	Gln	Pro	Glu	Ala	Leu	Ala	Ala	Ala	Ala	Ala
1			5			10			15						
Asn	Leu	Gln	Gly	Ile	Gly	Thr	Thr	Met	Asn	Ala	Gln	Asn	Ala	Ala	Ala
	20				25				30						
Ala	Ala	Pro	Thr	Thr	Gly	Val	Val	Pro	Ala	Ala	Ala	Asp	Glu	Val	Ser
	35				40				45						
Ala	Leu	Thr	Ala	Ala	Gln	Phe	Ala	Ala	His	Ala	Gln	Met	Tyr	Gln	Thr
	50				55				60						
Val	Ser	Ala	Gln	Ala	Ala	Ala	Ile	His	Glu	Met	Phe	Val	Asn	Thr	Leu
	65				70				75				80		
Val	Ala	Ser	Ser	Gly	Ser	Tyr	Ala	Ala	Thr	Glu	Ala	Ala	Asn	Ala	Ala
			85						90				95		
Ala	Ala	Gly													

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Asp Pro His Ala Met Arg Asp Met Ala Gly Arg Phe Glu Val His
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Mycobacterium tuberculosis

(xii) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Arg Asp Met Ala Gly Arg Phe Glu Val His Ala Gln Thr Val Glu
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Mycobacterium tuberculosis

(xii) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Arg Phe Glu Val His Ala Gln Thr Val Glu Asp Glu Ala Arg Arg
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Mycobacterium tuberculosis

(xii) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Ala Glu Thr Val Glu Asp Gln Ala Arg Arg Met Trp Ala Ser Ala

1 5 10 15

127 INFORMATION FOR SEQ ID NO: 38:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(11) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Mycobacterium tuberculosis*

(*1) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Asp Glu Ala Arg Arg Met Trp Ala Ser Ala Gln Asn Ile Ser Gly
1 3 10 15

(2) INFORMATION FOR SEC ID NO: 19:

(4) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(11) MOLECULES TYPE: peptide

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Met Trp Ala Ser Ala Gln Asn Ile Ser Gly Ala Gly Trp Ser Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

144 MOLECULE TYPE: peptide

(A) ORGANISM: Mycobacterium tuberculosis

(x1) SEQUENCE DESCRIPTION: SMO ID NO:40:

Gln Asn Ile Ser Gly Ala Gly Trp Ser Gly Met Ala Glu Ala Thr
4 5 10 15

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Ala	Gly	Trp	Ser	Gly	Met	Ala	Glu	Ala	Thr	Ser	Leu	Asp	Thr	Met	Thr
1				5					10					15	

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Met	Ala	Glu	Ala	Thr	Ser	Leu	Asp	Thr	Met	Ala	Gln	Met	Asn	Gln
1				5				10					15	

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Ser	Leu	Asp	Thr	Met	Ala	Gln	Met	Asn	Gln	Ala	Phe	Arg	Asn	Ile
1				5				10					15	

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iv) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Ala	Gln	Met	Asn	Gln	Ala	Phe	Arg	Asn	Ile	Val	Asn	Met	Leu	His
1			9					10					15	

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iv) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Ala	Phe	Arg	Asn	Ile	Val	Asn	Met	Leu	His	Gly	Val	Arg	Asp	Gly
1			5					10					15	

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iv) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Val	Asn	Met	Leu	His	Gly	Val	Arg	Asp	Gly	Leu	Val	Arg	Asp	Ala
1			5					10					15	

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Gly	Val	Arg	Asp	Gly	Leu	Val	Arg	Asp	Ala	Asn	Asn	Tyr	Glu	Gln
1				5					10				15	

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Leu	Val	Arg	Asp	Ala	Asn	Asn	Tyr	Glu	Gln	Gln	Glu	Gln	Ala	Ser
1				5				10					15	

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Asn	Asn	Tyr	Glu	Gln	Gln	Gln	Gln	Ala	Ser	Gln	Gln	Ile	Leu	Ser	Ser
1				5				10					15		

(2) INFORMATION FOR SEQ ID NO:50:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Met	Ala	Ser	Arg	Phe	Met	Thr	Asp	Pro	His	Ala	Met	Arg	Asp	Met	Ala
1					5			10					15		
Gly															

(2) INFORMATION FOR SEQ ID NO:51:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Met	Thr	Ile	Asn	Tyr	Gln	Phe	Gly	Asp	Val	Asp	Ala	His	Gly	Ala
1					5			10					15	

(3) INFORMATION FOR SEQ ID NO:52:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Gln	Phe	Gly	Asp	Val	Asp	Ala	His	Gly	Ala	Met	Ile	Arg	Ala	Gln
1					5			10					15	

(2) INFORMATION FOR SEQ ID NO:53:

(1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Asp	Ala	His	Gly	Ala	Met	Ile	Arg	Ala	Gln	Ala	Ala	Ser	Leu	Glu
1				5				10					15	

(2) INFORMATION FOR SEQ ID NO:54:

(1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Met	Ile	Arg	Ala	Gln	Ala	Ala	Ser	Leu	Glu	Ala	Glu	Ala	Gln	Ala
1				5				10					15	

(2) INFORMATION FOR SEQ ID NO:55:

(1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Ala	Ala	Ser	Leu	Glu	Ala	Glu	His	Gln	Ala	Ile	Val	Arg	Asp	Val
1				5				10					15	

(2) INFORMATION FOR SEQ ID NO:56:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(xii) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Ala	Glu	His	Gln	Ala	Ile	Val	Arg	Asp	Val	Leu	Ala	Ala	Gly	Asp
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(xii) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Ile	Val	Arg	Asp	Val	Leu	Ala	Ala	Gly	Asp	Phe	Trp	Gly	Gly	Ala
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(xii) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Leu	Ala	Ala	Gly	Asp	Phe	Trp	Gly	Gly	Ala	Gly	Ser	Val	Ala	Cys	Gln
1				5					10					15	

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

58

(B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Phe	Trp	Gly	Gly	Ala	Gly	Ser	Val	Ala	Cys	Gln	Glu	Phe	Ile	Thr
1				5				10					15	

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Gly	Ser	Val	Ala	Cys	Gln	Glu	Phe	Ile	Thr	Gln	Leu	Gly	Arg	Asn
1				5				10					15	

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

Gln	Gln	Phe	Ile	Thr	Gln	Leu	Gly	Arg	Asn	Phe	Gln	Val	Ile	Tyr	Glu
1				5				10					15		
Gln	Ala														

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 amino acids

(E) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Arg	Asn	Phe	Gln	Val	Ile	Tyr	Glu	Gln	Ala	Asn	Ala	His	Gly	Gln
1				5				10					15	

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Ile	Tyr	Glu	Gln	Ala	Asn	Ala	His	Gly	Gln	Lys	Val	Gln	Ala	Ala
1				5				10					15	

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Asn	Ala	His	Gly	Gln	Lys	Val	Gln	Ala	Ala	Gly	Asn	Asn	Met	Ala
1				5				10					15	

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids
(B) TYPE: amino acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Lys	Val	Gln	Ala	Ala	Gly	Asn	Asn	Met	Ala	Gln	Thr	Asp	Ser	Ala
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Gly	Asn	Asn	Met	Ala	Gln	Thr	Asp	Ser	Ala	Val	Gly	Ser	Ser	Tyr	Ala
1				5					10					15	

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Asp	Ala	His	Gly	Ala	Met	Ile	Arg	Ala	Leu	Ala	Gly	Leu	Leu	Glu
1				5				10						15

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Asp	Ala	His	Gly	Ala	Met	Ile	Arg	Ala	Gln	Ala	Gly	Leu	Leu	Glu
1				5				10					15	

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Met	Ile	Arg	Ala	Leu	Ala	Gly	Leu	Leu	Glu	Ala	Glu	His	Gln	Ala
1				5				10					15	

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Met	Ile	Arg	Ala	Gln	Ala	Gly	Leu	Leu	Glu	Ala	Glu	His	Gln	Ala
1				5				10					15	

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Ala	Gly	Leu	Leu	Glu	Ala	Glu	His	Gln	Ala	Ile	Ile	Ser	Asp	Val
1				5				10					15	

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Ala	Gly	Leu	Leu	Glu	Ala	Glu	His	Gln	Ala	Ile	Ile	Arg	Asp	Val
1				5				10					15	

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Ala	Glu	His	Glu	Ala	Ile	Ile	Ser	Asp	Val	Leu	Thr	Ala	Ser	Asp
1				5				10					15	

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Ala	Glu	His	Gln	Ala	Ile	Phe	Arg	Asp	Val	Leu	Thr	Ala	Ser	Asp
1			5					10					15	

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Ile	Phe	Ser	Asp	Val	Leu	Thr	Ala	Ser	Asp	Phe	Tyr	Gly	Gly	Ala
1				5					10				15	

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Ile	Ile	Arg	Asp	Val	Leu	Thr	Ala	Ser	Asp	Phe	Tyr	Gly	Gly	Ala
1				5					10				15	

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Leu Thr Ala Ser Asp Phe Trp Gly Gly Ala Gly Ser Ala Ala Cys Gln
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Phe Trp Gly Gly Ala Gly Ser Ala Ala Cys Gln Gly Phe Ile Thr
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Gly Ser Ala Ala Cys Gln Gly Phe Ile Thr Gln Leu Gly Arg Asn
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

Glu	Gly	Phe	Ile	Thr	Gln	Leu	Gly	Arg	Asn	Phe	Gln	Val	Ile	Tyr
1				5				10					15	

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

Val	Thr	Thr	Asn	Phe	Phe	Gly	Val	Asn	Thr	Ile	Pro	Ile	Ala	Leu	Asn
1			5				10						15		
Glu	Ala	Asp	Tyr	Leu	Arg	Met	Trp	Ile							
			20				25								

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Asn	Glu	Ala	Asp	Tyr	Leu	Arg	Met	Trp	Ile	Gln	Ala	Ala	Thr	Val	Met
1			5				10						15		
Ser	His	Tyr	Gln	Ala	Val	Ala	His	Glu							
			20				25								

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 967 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

```

TSAGGCGGAA CCTACGCGTC GGTTCGTCAC AGCGACCGCA TGGGCTGCTC CGCGGACTGC      60
CGCTAGGGTC GGGGATCACT CGGGGTAGCG GGGCTTTTGC CGACCGATAT GGTTCGCTC      120
ACAGTGTGGT TCGCGGCGCG CCATCGCGCG GATACGCGCA TGACCTCAGC TCGCGAGAAA      180
TGACATGCTT CCTAGAGGCG TGAGCACTCG AAGACACATA AGCAGGAGAT CGCATGCGCT      240
TTTGACTTAC CCAACAGAAA GCACTGCGCG CGCGGCGCGG CAGTCTGGCG GGAATCGGCT      300
CGGCATTGAA CGCGCAGAA TGGGCTGCGG CCACTGCGAC GACGAGGAGT GTCCGCGCGC      360
CGCCGATGAA NTGTCGCGCG TGACGCGCGG TCAGTTGCGG GCACACGCGC AGATCTATCA      420
GGCGGTGAGC GCGCAGCGCG CGGCGATTCA CAGATGCTTC GTCAACACTC TACGATGAG      480
CTCAGGCTGC TATGCTGCTA CGGAGCGCGG CACGCGGCGC GCGCGCGGCT AGAGGATCTA      540
CTCGGATGGA TTTGCGGCGG TTGCGCGCGG AGGTCAATTC GGTGCGGATG TATGCGCTTC      600
CTGGCTGAGC ACCATGCTTC GCTGCGCGCT CGGCTGGAAG CGGCTGCGG GCGGAGCTGA      660
GTTGCGGCGC CACGCTTAT GAGACGCTGA TCACTCAGCT CAGGAGTGGG GGTGAGCTTG      720
GTCCGCGCTC AGCGCGCATG GCGGAGCGCG TTGCGCGCTA TGTGCGGTTG ATGAGTGGCG      780
CTGCGCGCGC AGCGGAGCGG GCGGCGCACG AGCGGAGCGG CGTTCGCGCG GCTTTGAGG      840
CGGCTTTTGC CGCGAGCGTG GCTCGCGCGT TGATGCGCGG CAACCGGCGT TCGTTGATGC      900
AGCTGATCTC GACGAAATTC TTTGCTGAGA ACACCTGCGG GATCGCGCGC GCGGAGCTCT      960
AGTACGG

```

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

```

Met Ser Phe Val Thr Gln Pro Glu Ala Leu Ala Ala Ala Ala
1           5           10           15

```

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

```

Thr Gln Pro Glu Ala Leu Ala Ala Ala Ala Asn Leu Gln Gly
1           5           10           15

```

(2) INFORMATION FOR SEQ ID NO:86:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(11) MOLECULE TYPE: peptide

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:86:

Leu	Ala	Ala	Ala	Ala	Ala	Asn	Leu	Gln	Gly	Ile	Gly	Thr	Thr	Met
1					5				10					15

(2) INFORMATION FOR SEQ ID NO:87:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(11) MOLECULE TYPE: peptide

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:87:

Ala	Asn	Leu	Gln	Gly	Ile	Gly	Thr	Thr	Met	Asn	Ala	Gln	Asn	Ala
1					5				10					15

(2) INFORMATION FOR SEQ ID NO:88:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(11) MOLECULE TYPE: peptide

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:88:

Ile	Gly	Thr	Thr	Met	Asn	Ala	Gln	Asn	Ala	Ala	Ala	Ala	Ala	Pro
1					5				10					15

(2) INFORMATION FOR SEQ ID NO:89:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(11) MOLECULE TYPE: peptide

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:89:

Asn Ala Gln Asn Ala Ala Ala Ala Ala Pro Thr Thr Gly Val Val
 2 5 10 15

(2) INFORMATION FOR SEQ ID NO:90:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(11) MOLECULE TYPE: peptide

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:90:

Ala Ala Ala Ala Pro Thr Thr Gly Val Val Pro Ala Ala Ala Asp
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:91:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(11) MOLECULE TYPE: peptide

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:91:

Thr Thr Gly Val Val Pro Ala Ala Ala Asp Glu Val Ser Ala Leu
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:92:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(11) MOLECULE TYPE: peptide

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:92:

Pro Ala Ala Ala Asp Glu Val Ser Ala Leu Thr Ala Ala Gln Phe
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:93:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

Glu	Val	Ser	Ala	Leu	Thr	Ala	Ala	Gln	Phe	Ala	Ala	His	Ala	Gln
1				5				10						15

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

Thr	Ala	Ala	Gln	Phe	Ala	Ala	His	Ala	Gln	Met	Tyr	Gln	Thr	Val
1				5				10						15

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

Ala	Ala	His	Ala	Gln	Met	Tyr	Gln	Thr	Val	Ser	Ala	Gln	Ala	Ala
1				5				10						15

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

Met	Tyr	Gln	Thr	Val	Ser	Ala	Gln	Ala	Ala	Ala	Ile	His	Glu	Met	Phe
1				5				10						15	

(2) INFORMATION FOR SEQ ID NO:97:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

Ser	Ala	Gln	Ala	Ala	Ala	Ile	His	Glu	Met	Phe	Val	Asn	Thr	Leu
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:98:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

Ala	Ile	His	Glu	Met	Phe	Val	Asn	Thr	Leu	Val	Ala	Ser	Ser	Gly
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:99:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

Phe	Val	Asn	Thr	Leu	Val	Ala	Ser	Ser	Gly	Ser	Tyr	Ala	Ala	Thr
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:100:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

Val Ala Ser Ser Gly Ser Tyr Ala Ala Thr Glu Ala Ala Asn Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

Ser Tyr Ala Ala Thr Glu Ala Ala Asn Ala Ala Ala Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1784 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

```

ATTGCTTCCT GCGGCAGCTA AATCCCGGGG ACATGGTGGC GGGCCAGTAC GAGGTCAAAG      60
GCTGATCTCC GCACGGGGGA CTGGGCTGGA TCTACCTGGC TCTGACCCGC AATGTCALAG      120
CGGCTCCGGT GGTGCTCAAG GCGCTGTGTC ATTCGCGTGA TGGCGAAGCG CAGGCAATGG      180
CGATGGCGGA AGCCGATTG CTGGCCGAGG TGTTGCACCC GTGGATCGTG CAGATCTTCA      240
ACTTTGTGCA GCACACCGAC AGGCACGGGG ATGCGGTCGG CTACATCGTG ATCGAATACG      300
TCGGCGGGCA ATGCTCTAAA CGCAGCAAGG GTCAAAATCT GCGGCTGCGG GAGGCCATGG      360
CCTACCTGCT GGAGATCTGT CGGCGGCTGA GCTACCTGCA TTGCAATGGG TTGGTCTACA      420
ACGACCTGAA GCGCGAAAGC ATCATGCTGA CCGAGGAACA GCTCAAGCTG ATCGACCTGG      480
CGCGGATATC GCGGATCAAC TGTTGGGCT ACCTCTACGG GACCCGAGGG TTCCAGGCGC      540
CGGAGTGGCT CGGACCTGGT CCGACGGTGG CCACCGACAT CTACACGGTG GGAAGCGAGC      600
TCGCGCGGCT CACGCTGGAC CGAATGGCGG TTAATGGGAT GGGCTACCTG      660
AAGACGAGCC GGTGCTGAAA ACCTACGACT GTTACGGCGG GTTCTGCGCG AGGACCATGG      720
ATCCCGATCC GCGCAACCGG TTGACCCCGG CCGAAGAGAT GTTCGCGCAA TTGAAGGGCG      780
TGTTGAGGAA GGTGCTGACC CAGACACCGG GGTGCGCGCG CGAGCTATGC AACGATCTTC      840
AGTCCCACTG GGTGACATTT TGAGATGGAC TGCTGCTGGC GCACACCGAC GTGTATCTGG      900
ACGGCGAGGT CAGCGCGGAG AAGCTGACCG CCACAGAGAT CCGTGAAGGAT GTTCGCTGCG      960
CGGTGCTGCA TCGACACCGAC GTTGAGCTTT GGTGCTTCCA GGCACGGGTC GTCTCCGAGC      1020
CGGTCGACAC CTTAGACTCG GTGGGCGCGG CCGGCGACCG TGACCTGAGC GCTGACGGCG      1080
TCGATTTTTC TGTTGCTGCG AGCTGCGGCT AATGGAAGTG CCGCGGCTGG TGGATCTCGG      1140
CGATTTGTCG AAGGCGCACG GAAAACTGGA CGATCTGGCC GAACCGCTTG GGTGGCGATG      1200
CGGATGAGTC TGTTACCGCG CGTTCGCGGA GCTGCTCAGC GCGGACTATG ACTGCGCCAC      1260
CAACGATTTC ACCGAGGTGC TGGATACCTT TCCGCGGAGC CTGGCGGCTCA AGCTCGGCTT      1320
GTCGCTTACC CGGGAACTAG CCGGCAACAC CGACGAACAC AAGTTCATAT AGACGGTGTG      1380
GAGCAGCAAG GAGCGCAGAG TCTCGGCGGC TTGTGGACTG GCGAGAGCTC GTCGAGCGGA      1440
AGGTGATCGG GTGCGGCGCG TGCGCAGGCT GAGGAGATTA CCGGCCACTT CTGCGGCAAT      1500

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CACCACGGCA	CGGCTGACCA	GCSCGGTGAC	TCTGTTGTCC	GGCCGGTCAA	CGAGTGAAAT	1560
CACCGAGGAA	CAGATCCGCG	ACSCCGCCCG	AAGATGTGAJ	GGCTGACCC	CGACCGAATC	1570
ACGCGTGCTG	CAGATCCGCG	CCCTGGTGCT	GGGTGGGCGC	CTGGACTGGC	TGAAGGACAA	1580
CAGCGCCAGC	ACCAACACCA	TCTTCGGTTC	CCGTTTCAAC	ACTGACGGGC	TCCGCTGGG	1590
TGTGAGGCG	TCACTGGCCA	CCCTGGCCCG	GTTAGCTCCC	ATCC		1784

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 766 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

ACAACACACT	CGGTGACGC	CGMTCCGGCC	TGATCGTCCG	TGATCAAGCTT	CGTCCCAAT	60
TGGGCAACAG	GTGCGCGCT	CCCAAGAGAT	TCTTCGCGC	AGTTCGCGC	KAATTAAGCTT	120
ATGCTGCTTG	GGTCCCGCTC	CCCAACACCC	CGGAACCTTA	ACCAATTTTA	ACCGGCGAGG	180
AAGTTTCTTA	CATTTACCCN	GGGMAACCAA	CCGGGCGCTC	MAAAATCCG	TCTTGGAGCT	240
CGAGCGCTTC	CCGTGCTTC	CCGCACTGCT	GACCGGCAAG	GATATCGCG	AGCGCGCGTT	300
GGCCAAACCG	TGATGCAAC	TGGCTTACCG	TGCGACCAAG	GACCGCATCA	CCGGCTGGGA	360
GTCCGACCAAG	GTACTGCAAT	CTGGCGACCA	CACCAAGCAAG	CAGACCAAGC	TGGTCCAGCG	420
CGATTTCCAG	CCCGCGCGCG	CCGCTGCTAT	ACGATTTGGT	CGAAGACCAAT	CCGAGGAGAT	480
TCATCAAGGA	CGGTCAAGGA	AAGCGATCGC	CCCAATGGG	GGACACCCCN	AGCCAGGCGN	540
ATTACCGGTT	NAACAGATTG	GGTATGGTTC	TTTATATATG	AKCAACCCAT	AGCGAGCGG	600
CCCGCGAATG	GTAGACCAAG	ACCACTGCCC	CCAGTTGCTG	CACCAATTTG	ATGATCCGCG	660
CGGATCGGCT	GACCGCGCGC	AGCGTTCCCG	ATGCGGAGAT	GAGCGTGAAC	AGCCGCGTTG	720
ACCTGTTGAT	CGAGTTTTC	CAGTGGCAAG	TGGCGAGCTG	CCCGCT		766

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1231 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

CGGCACGAGA	ATGTCGCGCT	TGCTTCGATA	GGCACTTGGC	TGTGGTCCCG	CTGCGACCGG	60
GTGACGACAG	TGGCTCGGCT	CAGGCGCATG	GGCGCGCGCG	GGAGCGCGAT	GTGCGCGAGA	120
CCCGGTGTAC	GAGAACCGGA	CTCGACCAAG	TGTCGGCGCT	GACGCGCGCT	CGATTCGCGG	180
CACGCGCCCA	GATCTATCAG	GGCGTCAGCG	CCGAGCGCGC	GGCGATTCAC	GAGATGTTCC	240
TCAGACTCT	ACAGATTAAC	TGAGGCTGCT	ATGCTGCTAC	CGAGCGCGCG	AACCGCGCGC	300
CGGCGCGCTA	GAGGAGTCAAC	TGCGATGGAT	TTTGGGCGCT	TGCGCGCGCG	GGTCAATTCC	360
GTGCGCGAT	ATGCGCGTTC	TGCTCGGCA	CCCAATGCTG	CTGCGCGCTC	GGGCTGGGAC	420
GGGTGCGCG	CGAGCTGAG	TTGCGCGCG	ACCGGTTATG	AGAGGCTGAT	CATCTAGCTC	480
ACGAGTGAAG	GCTGCGTAG	TGCGCGCTCA	CGCGCGATGG	CCGAGCGAGT	TGCGCGGAT	540
GTGCGTGA	TGAGTGGCG	TGCGCGCGCA	CGCGAGTCAAG	CGCGCACAGC	GGCGCGCGCG	600
CGCGCGCGCG	GTGTTGAGCG	GGGTGTTGCT	GGAGCGGCTG	CTGCGCGCTT	GATTCGCGCG	660

AACCGGGGCTT	CGTGTATGCA	GCTGATCTCG	ACGAATGTCT	TGGTTCAGAA	CAGCTCGGGG	720
ATCGCGGCGG	CGGAAGCTCA	GTACGGGGAG	ATGTAGGGCG	AAGACTTCCG	GGCGATGTAT	780
GGCTACCGCG	GCAGTTGCGG	GAGCGGCTCG	GGGGTCAGCG	CGTTTAGCAC	GGCGGCGCAG	840
ATTGCGCAAC	CGACCGCTCA	GGGTACGCAG	GGCGCGCGCG	TGGCCACCGC	CGCGGTTACG	900
GGCGACTGGA	CGCTACGGGA	GATGATCAAC	GGGTACCGCA	AGCGCTTCCA	AAGCGTCAAC	960
TCACNTCTGT	TGCAGTGTCT	TAACTGTGCG	CTGTCTGTGG	TGTGGCAGAT	CTTGTGTGGG	1020
ACGCGCAATT	TCCGCACTTC	AACTTCGGCA	CTGCTGACCG	ACCTGACGCG	CTACGCGGAG	1080
TGTTTNTATA	ACACCGAGGC	CGTGCCTATC	TTGAGCATCG	GCATGGGGCA	CAGCTTCATT	1140
CAGTGGGGCA	AGACCTCTGG	ATGATCTGGG	TAGGGGCGAC	CGGCTGCGGT	CGCGGTTGCT	1200
GGGAGTNGCG	CGAAGGCGCT	CGCTCTGCGC				1260

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (a) LENGTH: 2041 base pairs
- (b) TYPE: nucleic acid
- (c) STRANDEDNESS: single
- (d) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

CGGACGGGCG	TGGTCCGAT	CAGTCCCAT	GACGGCTTCT	ACGACCTTCT	GGGAGTTGGA	50
ATACCCAAAC	AAGGGGGTAT	CGTTTACTCC	TCACTAGAGT	ACTTCGAAAA	AGCCCTGGAG	120
GAGCTGGCAG	CAGGCTTTCC	GGGTGATGGC	TGGTTAGGTT	CGGCGCGGGA	CAATATAGCC	180
GGCAGAAACG	GCACGCAAGT	GAATTTTTC	CAGGAGCTGG	CAGGCTCGGA	TGCTCAGCTC	240
ATGAGCTTGA	TCCAGCACTA	GGCCAAACGC	GTCCAGAGCA	CGCCCGACAT	CTGGGAGGCG	300
GGCAGAGAAAG	GTCTCGAGTT	CGTGGCGCGG	GTGGCTGTGG	ACCTGACTTA	CATGCCGGTC	360
GTGGGACAGC	CGCTATGGGC	CGGCTTCCAN	GCGCGCTTTT	GGGCGGCGCG	GATGCGCGTA	420
GTGGGCGGCG	CGCTTGGCTA	GTGGTGGTGG	AAACCGCTGA	TCAACCGGAC	TCAACTCTCT	480
AAATTCCTTG	CCAAATTGGC	GGAGTTGGTC	GGGCGCGCCA	TGGCGGACAT	CATTTCGGAT	540
GTGGCGGACA	TGATCAAGGG	CATCTTCGGA	GAAGTGTGGG	AGTTTCATAC	AAACGCGCTC	600
AAGGCGCTGA	AAGAGCTTTT	CGACAAGCTC	ACGGGATGGG	TGACCGGACT	GTCTCTCGGA	660
GGGTGCTTGA	ACCTGGAGTC	CTTCTTTGGC	GCGCTTCCCG	CGTTTACCGG	CGGAGCCAGC	720
GGCTTTCGCG	AAGTGAATCG	CTTGTTCGGT	TGGCGCGGCT	TGTCGCGATC	GTGCGGCTTG	780
GCTCAGCGGG	ATAGGCTTGG	GAGCTCAGCG	AGCTTTCGCG	CGCTGCGCGG	CATTGGCGCG	840
GGGTCGGGTT	TGGGCGGCTT	CGCGAGCTTG	GCTCAGGTC	ATGCGCGCTC	AACCTCGGAG	900
GGCTACGGAG	CGCGAGCTGA	TGGCGCGGTC	GGCGCGCGCT	CGGAGCGGCT	CGGCGGCGAG	960
TGCGGAGCTG	TCTTGGCGCA	GGTTCCTCAA	GGTATGAGCG	GACCGCTAGG	CATGGGGTGC	1020
ATGCACCGCT	CTTCCGCGCG	GTGGAAGGGG	ACUACGACGA	AGAAGTACTT	CGAAGCGCGC	1080
CGCGCGCGCA	CTGAGAGCGC	CGAGCGCGCG	CCAGTGGAGG	CTGACGCGGG	GGGATGGGCA	1140
AAGTGTCTGG	TAGCAAAAGT	CGTCTAAGCG	CATGGCGAGG	CAATATCATT	GTGAGCGCAG	1200
GGCTTAACAG	GGCAATATCT	AAACCGAGGG	GACACGGATCA	ATGACGGGAA	ACTTGAACGT	1260
CGAGCGGAGG	CGTCTTGGTG	TACTTGGGTC	GCACCATGAC	AACCGCGGCG	TGTAATGCTG	1320
CTGGGCGGCT	GAGGCTGCGG	CTGGGCTAGG	CGAATCTGTT	CGGATCACTC	ACGGTCTGTA	1380
CTGCTCAGAG	TTCACAGACA	CGTTAAATGT	GTACTTGACT	GGCCACAAAT	CGTTGGGCTC	1440
GTCTTTGAGT	ACGCGCGGTT	TGATCTGTGG	CAAAAGCTTT	CGAATCTGCG	CGAAGATATA	1500
TAGCGAGGCG	GACCAAGCGT	GGCGCAAGGC	TATCGACGGA	TGTGTTTACT	GACCAAGCTT	1560
GCTTCGCGCA	CGTGAAGGCC	CGACCTAGGG	CAGGTCGCTG	CGCTTCTTAG	CGTGAAGGCG	1620
ACCGCTAGAG	ACCGAGCGCC	GGTTCGCACT	GATGGGCAAG	GACAGTAGCT	CGCCGCGCAT	1680
CGCGGCTGCG	GTTCGCGGCA	CAAACTCGGG	CAGTTCGCGG	TGCGGCAACA	CGGTGCTGGG	1740
GGAGCCCAAG	CGCGCAAGCG	CGGATTAACA	TGCGGACCGC	AGCAGAGCGG	AGAGCTCATG	1800
TTGTCGAGAT	CGGCTGCGGT	CAGCGATGAG	CTGGCGGCGC	GGCGGAGGCA	GTGTTGTGGG	1860
ATCGGCGGCG	GGGTGAGGCA	CAGTGGGCGA	GCTTAACCTA	CGCTCTCGCC	GGGAGAGCGG	1920

TCCTTGTCTGA	TAAGATACCTG	CGAGCATGCC	AGCAGCGAGC	GCATCCGACC	GGGTGAGGA	1980
ATTGTCGGG	CGCTCTGATG	CGAGCTTGT	CGAGCTTGT	CATGCCATCC	ACCTGCTGC	2040
G						3041

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1302 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

GAGCTCAGCG	CTATCAACCA	ATACITTTTG	CACITCAAGA	TGCAGGACAA	CTGGGTTT	40
ACCAGCTCTG	CGGCGCACAC	CCGCGCGGAG	TGCTTCGAGC	AAATGCGCCA	CGCCGAGGAA	120
ATTACCGATC	GCATCTTCTT	GCTGGATGCT	TGCGGAACT	ACCAGCGCAT	CGGTTCCTTG	160
CGTATCGGCC	AGACGCTCCG	CGAGCAATTT	GAGGCGGATC	TGGCGATCCA	ATACGACCTG	240
TTGAATCGTG	TCAAGCGGAG	AATCCTCATG	TCCCGGAGAG	AACGAGACAC	CACCCAGCCC	300
GTACTGCTTG	AGAAATCGT	TGCCGAGGAG	GAGGAACACA	TGCACTACTT	GGAAACGCGG	360
CTGGAGTCTA	TGGACAGCT	AGGAGAGGAG	CTTTACTCGG	CGGAGTCTGT	CTCTCGCCCA	420
CCGACCTGAT	CGCCGCTTGA	GGATTCCTCG	ATACCTACTC	GGGCGCGGCT	GACAACTCTT	480
AGCATCGACT	GAAACAGCGA	TGGGAGGCGG	GATATCGCGG	GGCCGACAGC	ACCGACCACT	540
GGCCCGACCG	CAATCGGAGC	CGGTGGCGCG	CTGCTCACTC	CGGTGGGAGC	CACCAATTAT	600
TTCAAGCGAC	TTGTCTTCTG	GGTCTCTGCT	GCTGCGGAGC	GCCAAACCAT	CGTGTGCGCC	660
GCATTGCGGA	CGATCTGTCG	CGAGCTGGGG	AGCAGCGCTG	ACCACTCGTG	GGCGGTCAAC	720
AGCTATCTCG	TGGGGGGAAC	ACTSKYGNKK	KTGKGGKSKS	KKMMMECTC	GGTATCTGCG	780
TGGGCGGCAA	CAGGGGCTGT	CTAGGCTCTG	TGCTGCTCTT	CGTCTGCTGC	CTGTGCTGCT	840
CGGGTTATC	CGAGAGCATG	ACCACTGCTG	CGATCTCTCG	CGCACTGCAG	GGGCTGCTGT	900
CGGTGCGGAT	TTCTGCTCAC	GGTACGCGCG	TGGCGCTGTA	GGTGTCTCCA	CTCGGGGACC	960
GTGGCGCGTA	CGAGGGGCTG	TTAGTCTGCG	TGTTCTGCTG	CAACAGCGTC	ACCGGTTCGG	1020
TGCTGGGGGG	CTGGCTCACG	GACTATCTGA	GCTGGGGGTTG	GGCGTTCCGA	CGACCAAGCC	1080
CATCAAGGAC	CGGATGCGCG	TCTGCGCGCG	GAAACAGGCG	CTCGCGCGGT	TGCGGGGAGG	1140
TCCCTTGGGG	AAGTGTGCTC	CACAGGCCCA	GAACTGTGAG	AAATCGGATG	GGCGAGCCAC	1200
AC						1202

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 496 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

GGCGGCGCCA	GTTCGCGCAG	AGTTNGCGCG	GGGGAGCGCG	TTGCGGAGCC	AGAAATCTCG	60
CGTGGGCAAG	CAGCGGGGAG	CGGCGGACCT	CGTCACTTNG	GATCGCGCGG	ACCGCGCGCG	120
ACCAAGGCCA	TTCCGCGGCT	GAGGAAGTCT	GAATNTCTCG	CAGTATGATC	GGCTGCTGCG	180
AACGCTCTCC	GGATTGCGGA	GGGATCTGCG	GGCGAGGCTC	GGTCTCTCAG	ACCGCGGAGC	240
ACCGCTACNG	ACAGGCGCGC	ATAGCTGAAT	GACCGCGGCT	NACCGCGGCT	CGTCTCTCAG	300

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NGAATATGGCC CCGGANGCAA AGATCCGTC GGGCTCCGC CTCGGCGACG ACAGCCACCT 360
TCACCGCGGC GTTATCCGTC GCGCGATCG CAIACCGGC GCGCTCAAGG TCGCGCTTGC 420
GGTAGTCACG CACCGACAAG GCGATVTCG CCGTGGCTTG GACGGGCGGG GTGACGCTGC 480
GGGCGATCAM GTCCAC

```

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 849 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

```

TGGATTCGGA TAGCGGTTTC GGGCCCTCGA CCGCGGACGA CCGCGGCGAG GCTCCGAC 60
GGGGGGCGCG GACGCTGGGA TTCGCGCGGA CCGCAACCAA AAAACGCCAG GTCCGGCGCG 120
TGGGCTGAC CCGACTGGCC GGTGATGAGT TCGGCAACCG GCGCGGATG CGGATGGTGC 180
CGGGGACCTG GAGGACGGGC AGCAGCGAGC CCGAGCGGCT CCGACGGATG GCGAGAGGCG 240
GAGGCGAAGG GTTACCGCAC GACAGCAAGT AACCGAATTC CGAATCACCT GGACCGGTAC 300
GGGTGGAAGG GAGAGATGTT ATGAGCGCTT TGGATGCTCA TATCCACAG TTGCGGGCTT 360
CCGAGTCGCG GTTTCGCGCC AAAGCGGCGG TGATCGGCG CCGATCGGCT CAGCGCGAGC 420
AGGCGCGGAT GTCGGCTCAG CGGTTTACG AGCGCGAGTC GTCCGCGGCG TTTCAGCGCG 480
CCCATCGCCG GTTGTGGCG GCGCGCGCGA AAGTCAACAC TTGTTGGAT GTCGCGCAGG 540
CGAATCTGGG TGAGGCGCGC GGTACCTATG TCGCGCGCGG TCGTGGCGCG GGTTCGACCT 600
ATACCGGTT CTGATCAAC CTTCTGACG GAGAGGACTT GTGATGTGCG AATCACTATA 660
CACTACGCGC GCGATCTTGG GTACCGCGCG GCGATATGCG GATATGCGCG CACCGCTGCA 720
GAGCTGGGCT GCGGAGATCG CCGTGGAGCA GCGCGGCTTG CAGAGTGCCT GCGAGGCGCA 780
TACCGGATG ACGTATCAGG CBTGGCAGCG ACANTGATAA CCGCGCGCAG GAGGATTGG 840
TSCGGGCTT

```

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

```

Met Ser Leu Leu Asp Ala His Ile Pro Gln Leu Val Ala Ser Gln Ser
1           5           10           15
Ala Phe Ala Ala Lys Ala Gly Leu Met Arg His Thr Ile Gly Gln Ala
20           25           30
Glu Gln Ala Ala Met Ser Ala Gln Ala Phe His Gln Gly Glu Ser Ser
35           40           45
Ala Ala Phe Gln Ala Ala His Ala Arg Phe Val Ala Ala Ala Lys
50           55           60
Val Asn Thr Leu Leu Asp Val Ala Gln Ala Asn Leu Gly Glu Ala Ala
65           70           75           80

```

Gly Thr Tyr Val Ala Ala Asp Ala Ala Ala Ala Ser Thr Tyr Thr Gly
 65 90 95
 Phe

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

Met Ser Leu Leu Asp Ala His Ile Pro Gln Leu Val Ala Ser Gln
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

Ala His Ile Pro Gln Leu Val Ala Ser Gln Ser Ala Phe Ala Ala
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

Leu Val Ala Ser Gln Ser Ala Phe Ala Ala Lys Ala Gly Leu Met
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

Seq	Ala	Phe	Ala	Ala	Lys	Ala	Gly	Leu	Met	Arg	His	Thr	Ile	Gly
1				5			10						15	

(2) INFORMATION FOR SEQ ID NO:114:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

Lys	Ala	Gly	Leu	Met	Arg	His	Thr	Ile	Gly	Gln	Ala	Glu	Gln	Ala
1			5				10					15		

(2) INFORMATION FOR SEQ ID NO:115:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

Arg	His	Thr	Ile	Gly	Gln	Ala	Glu	Gln	Ala	Ala	Met	Ser	Ala	Gln
1			5				10					15		

(2) INFORMATION FOR SEQ ID NO:116:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

Gln	Ala	Glu	Gln	Ala	Ala	Met	Ser	Ala	Gln	Ala	Phe	His	Gln	Gly
1			5				10					15		

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

Ala	Met	Ser	Ala	Gln	Ala	Phe	His	Gln	Gly	Gln	Ser	Ser	Ala	Ala
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

Ala	Phe	His	Gln	Gly	Gln	Ser	Ser	Ala	Ala	Phe	Gln	Ala	Ala	His
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

Gln	Ser	Ser	Ala	Ala	Phe	Gln	Ala	Ala	His	Ala	Arg	Phe	Val	Ala
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

Phe Gln Ala Ala His Ala Arg Phe Val Ala Ala Ala Lys Val
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

Ala Arg Phe Val Ala Ala Ala Lys Val Asn Thr Leu Leu Asp
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

Ala Ala Ala Lys Val Asn Thr Leu Leu Asp Val Ala Gln Ala Asn
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

Asn Thr Leu Leu Asp Val Ala Gln Ala Asn Leu Gly Glu Ala Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

Val Ala Gln Ala Asn Leu Gly Glu Ala Ala Gly Thr Tyr Val Ala Ala
1 5 10 15
Asp Ala

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1752 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

CGGACAGAGA	ATGTGCGCTT	TGGCTCGATA	GCGACTTCCG	TGTGGTCGGG	CTCCGACGGG	60
GTGAGCCAGG	TGGCTTGCTC	CAGGCGCATG	GCCGCGGCGA	GGAGGCGGAT	GTGAGCCAGA	120
CCCGGTGTAC	GAGAACCGGA	CTCGACNAG	TGTGCGGCTT	GACCGCGGCT	CAGTTGCGGG	180
CACACGCCCC	GATCTATCAG	GCGCTCAGCG	CCGAGGCGGT	GGGATTCAC	GAGATGTTGG	240
TGACACACTT	ACGATNANC	TGAGGTGCT	ATGCTGCTAC	CGAGGCGGCT	AACCGCGCGG	300
CGGCGGCTTA	GAGGAGTCAC	TGCGATGGAT	TTTGGGGCGT	TGGCGCGGGA	GTCATATTCG	360
GTGGGATGTT	ATGCGGTGTC	TGGCTCGCGA	CGAATGTTG	CTGCGGCGTC	GGCTCGGAAC	420
GGGTGTGGCG	CGGAGCTGAG	TTGCGCGGCT	ACGGATTATG	AGAGGTTGAT	CATCTAGCTC	480
AGCATGAGGG	GTTGCTTAGG	TCCGCGCTCA	CGCGGATATG	CCGAGGCGAGT	TGCGCGGTAT	540
GTGGCGTGGA	TGAGTGCCTG	TGCGGGCGCA	GCGGAGCAGG	CGGCGACACA	GCGCGAGGCG	600
CGCGCGCGCC	CTTTTGAAGC	GGGTTTGCC	CGGACCGTGC	ATCGGCGGTT	GATCGGCGGC	660
AACCGGCTTT	CGTTGATGCA	GCTGATCTCG	ACGATGTGCT	TTGCTCAGAA	CAGCTCGCGG	720
ATCGCGCGCG	CCGAGAGTCA	GTACCGCGAG	ATGTGGGCGC	AAGACTCGCG	GGGATGTGAT	780
GCTTACGCGG	CGAGTTGCGG	GAGCGGCTCG	GGGTTCAGCG	CGTTTAGCGC	GCGGCTCGAG	840
ATTGCGACCG	CGGCGGCTCA	GGGTACCGAG	CGCGGCGCGG	TGGCTACGCG	CGCGGATACC	900
CGCCAGTCTG	CCTGTACCGA	GATGATCAGC	GGGTACCGCA	ACCGGCTGCA	AAGCTTCAGT	960
TCAGCTCTGT	TGCAATGCTC	TAGGCTGCTG	CTGTGCTGGC	TGTGGCGAGT	CTTGTTCGGG	1020
ACGCCCAATT	TCCGCACTTC	AATTTCGCGA	GTGCTGAGCG	ACCTGCGAGC	GTACCGCGAG	1080
TINTTNTATA	ACACCGAGGG	CCGCGGCTAC	TTGAGCATAT	GCATGGGCAA	CACCTTCTAT	1140
CAGTCGCGCA	AGACCTTGCG	ATTGATGCGG	TAGCGCGGAG	CGGCTCGGAT	CGCGGCTGCT	1200
GGGATGCGCG	CCGAGGCGTT	GCTTGGAGTG	GGCGGAGATC	TGCTTGGCGG	GCGGCTGGCG	1260
CGCGGCTGCG	CGAATGAGCG	TTGCGTGGCG	AAGCTGTGCG	TGCTGCGGCT	TGGGANTGGA	1320
CGCTTGGCGG	GCTCGGTGAC	TCCGCGGCGT	GCTGCGCTAC	CGCTGAGTAC	GCTCAGTGCC	1380
GCCCGCGAGG	CGCGCGCCCG	AAGCTTCTTG	GGCGGCTTGC	CGCTAGCTGG	TGCGGGCGGG	1440
CAGTCGCGCG	GTCAGCTTGG	CGGATTCGCT	CGGAGCTGCA	TGGCTTGGCG	ACCCCTTGCG	1500
GGGATGCTCG	CTGCGCGCAAC	GTATTAACGC	CGCGGCTTGC	GCTGTGTGCG	TGCGCTGCGG	1560
GTGCGAATGG	GTGCGCGCGG	AAATCTGCGT	GGGTTATTTT	CGGTGGGAGT	TTTCCCGGAA	1620
GCGCGCTTCA	GCACCGGATT	TCTTAAGGAT	CGCGCACTC	TGCTGCGGAA	TTGCGCACTA	1680
AGTAGCTGCG	GGCGGAAAGC	GTTTGGGTTT	GAAAGCTTCA	GAAAGCGCGG	CTCCAGAGGG	1740
TTGCGCAAGC	GG					1752

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

```

Met Asp Phe Gly Ala Leu Pro Pro Gln Val Asn Ser Val Arg Met Tyr
  1          5          10          15
Ala Gly Pro Gly Ser Ala Pro Met Val Ala Ala Ser Ala Trp Asn
  20          25          30
Gly Leu Ala Ala Glu Leu Ser Ser Ala Ala Thr Gly Tyr Glu Thr Val
  35          40          45
Ile Thr Gln Leu Ser Ser Gln Gly Trp Leu Gly Pro Ala Ser Ala Ala
  50          55          60
Met Ala Glu Ala Val Ala Pro Tyr Val Ala Trp Met Ser Ala Ala Ala
  65          70          75          80
Ala Gln Ala Glu Gln Ala Ala Thr Gln Ala Arg Ala Ala Ala Ala Ala
  85          90          95
Phe Glu Ala Ala Phe Ala Ala Thr Val Pro Pro Pro Leu Ile Ala Ala
 100          105          110          115
Asn Arg Ala Ser Leu Met Gln Leu Ile Ser Thr Asn Val Phe Gly Gln
 120          125          130
Asn Thr Ser Ala Ile Ala Ala Ala Glu Ala Gln Tyr Gly Gln Met Trp
 135          140          145
Ala Gln Asp Ser Ala Ala Met Tyr Ala Tyr Ala Gly Ser Ser Ala Ser
 150          155          160
Ala Ser Ala Val Thr Pro Phe Ser Thr Pro Pro Gln Ile Ala Asn Pro
 165          170          175
Thr Ala Gln Gly Thr Glu Ala Ala Ala Val Ala Thr Ala Ala Gly Thr
 180          185          190
Ala Gln Ser Thr Leu Thr Glu Met Ile Thr Gly Leu Pro Asn Ala Leu
 195          200          205
Gln Ser Leu Thr Ser Xaa Leu Leu Gln Ser Ser Asn Gly Pro Leu Ser
 210          215          220
Trp Leu Trp Gln Ile Leu Phe Gly Thr Pro Asn Phe Pro Thr Ser Ile
 225          230          235          240
Ser Ala Leu Leu Thr Asp Leu Gln Pro Tyr Ala Ser Xaa Xaa Tyr Asn
 245          250          255
Thr Glu Gly Leu Pro Tyr Phe Ser Ile Gly Met Gly Asn Asn Phe Ile
 260          265          270
Gln Ser Ala Lys Thr Leu Gly Leu Ile Gly Ser Ala Ala Pro Ala Ala
 275          280          285
Val Ala Ala Ala Gly Asp Ala Ala Lys Gly Leu Pro Gly Leu Gly Gly
 290          295          300
Met Leu Gly Gly Gly Pro Val Ala Ala Gly Leu Gly Asn Ala Ala Ser
 305          310          315          320
Val Gly Lys Leu Ser Val Pro Pro Val Trp Xaa Gly Pro Leu Pro Gly
 325          330          335
Ser Val Thr Pro Gly Ala Ala Pro Leu Pro Val Ser Thr Val Ser Ala

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CAGGTGCGCA	CTTTCAGGT	CTGATGGGTG	CGGTGATCC	TGCTCGGACT	CGCTGGCCG	900
GCTATCACT	GTAAGTCA	GATCTCTCT	AGCAGCTTGG	CGTCACTCTT	GAGTGTGATG	960
ATAGTGGCC	CGGCAGCTT	GTGGAATGCG	GGTTTGTGG	GGGCGAAAC	GGTGTACTCG	1020
CGCCCGTGA	GGGTTCGAC	CAGATTACAC	TCCGGGTTC	GCTTCCCGCA	CAGAGCCGAG	1080
GTGAGGTAC	TGAGCATCG	GTGTTTGGAA	GGCCGCTAG	CGACCTGGTC	TTGGGCCATT	1140
CGGCGCCAG	ATCCGCGACT	GGTGGGATT	TCCGCGGCT	ATTCCCGCCA	CGCACACCA	1200
ATCAGTCCG	CTGGGGTAC	CCATTTCGG	CGTGGTAACT	GGCTCCGCG	GGCTGATCG	1260
CGTTTCGG	CTGGTTCCT	CGACACGGG	TTTGGTCTC	GAACAACCG	CTAGAGACG	1320
AATCGGATG	GCTCGAGAG	TCCCTCTGC	GGCCGGTTT	GCTTGAACG	TGATCATCG	1380
TTGATTTCT	TTGCTTCTG	GGCGGGTGG	AACGCGCTC	TCTTGGGTG	A	1440

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

GCACGAGGT	CTATCTTT	CACCCAGCT	CCGTAGGAA	CGCTGGCT	CGCTAATCA	60
GATGCGGCG	GGCTTCGAT	CGAGAGTAA	CGGATCGCC	GGCAGCAAT	GGTATCCAC	120
CGAGCTGAT	TCCCGGCG	CGGCTTCCA	CGTATAAGG	CGGGTCTGG	CGATCTCGA	180
ACGGCTGAC	TACGAGACT	TCTCGGTAG	ACGTGACGA	CTTTACCGA	TTATCGCTGA	240
CGATCTTGC	CTCCCAAGG	TCCAGATCT	ACTGTGCT			279

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1470 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

ACGCCACCT	CGAGCGGGA	ATCACCTCG	GTAACTCGG	AATCCAAAT	CTTCATCGC	60
GGCTTCGGA	ACAGCGAAG	CGAGCCGAC	GGCTGATAG	CTTTTCTCT	GATGTTCCAA	120
CGCCCGGCG	CCTGGAAGA	AACGATAGA	CCCGCTCTT	GGGGGTGAA	CGCATGAAT	180
TGTGATGCG	CGAGCAAGG	CAGCGCGAG	AGACCTTGA	TCCGGGCGG	CAGATTGCA	240
CGACCACTA	TCCGCAAGG	GTGATTTTG	CGGCGAAGG	TGAGCGGAG	ACCTCGAGC	300
TTTCTGTAG	GGTCAATTT	CACGCTGAC	AGCGCGGCA	ACTCAAGCG	GACCGAGCC	360
GTGCGAGGA	TCCCGTAGG	GGGTAGTCA	TGGGTGAT	ACACCTTGG	CACATCAGC	420
CGAGAAATCA	TGTTCCCTT	CGTCAAGCG	CGGTACCTG	CGATGCAAG	ACCGCCGGG	480
TATTTGAGG	CGACATGCT	GGTGGCTGG	GGGCTTGG	CGTGGCGCT	TGGATGAGC	540
CGACCGGCG	TGATCTCTG	CGGCAAGAC	TCCGGGCTT	GGCGCGGCA	GAATCAAGT	600
GAAGAGAGAT	AGGTCTAGG	CGGTTTTC	AGAGAGTGA	TTAATGAGA	GGCATTCGG	660
CGACCGGCG	GTCTCTCTG	GGCTTTTGG	ACGTATCGG	GGACGAAGT	CTTGGGCTT	720
TCTTCGAGG	CTCTCTGAT	TTGCTGAGC	AGATCTCGG	TCTCTCTGT	CAGCTTTCT	780
CGACCTCTT	GGCCCGGCG	GGTCTCGCG	GGGATGCTT	GATCATGCG	GGCGGACCG	840

CCACGCTTGG	TCTGCTCTTG	CCCLATCCCC	GCTTCTGTCT	TCCTCATGSC	CTTTCAAAAG	908
CCCCCGGGTG	CGGTCACAC	CCCCGCTGTC	TTTCTCTGAC	CTACCGGTCA	ACACCAACGT	968
TTCCCGGCTG	AACGAGGCTT	AGGAGAGGCTC	AGCGGTCTAGT	TGCTCTACCA	GCTCCAGGGC	1028
ACTGTCCACC	GAATCCAGCA	ACGCAACCAAC	ATGGGCTTTA	CTACCCCGCA	ACGGCTCCAG	1088
CTTCCGGATG	CGAACCTAGC	AGTCCCGGCTC	AGGTCCGAAG	TCACCCGAGTC	CGAGCTTAGCC	1148
CGGCGGATAT	CAGCCCGGAA	CCGCGGAGAG	CATTTCGCTC	CGGAATACG	CGCGGGTGTG	1208
GCTCCCGGCT	TTTCCACCTG	ACTCAGCACC	TGGTGTTCG	GTACATTAAC	GCTTTATCGA	1268
GCCTCCGCGC	ACCAAGCGTT	TGTACAGGCG	CTTTCCTCAG	CGGACATCGG	AGTACTCGAG	1328
GTTCAGCAGG	TGCACCGGGG	GGCCGAGCCA	GCTCAGGTTG	TCCCGCTGCC	CGAAACCTTC	1388
GAGCAGCGCG	AGTTTGGCGG	GGCAGTCCAG	CAGTCCCGCG	CAATCCATCG	GGTCAAGCTC	1448
GAGCTGATCC	AGCAGGTGTG	CCCAGGTTTC				1478

(i) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1059 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

ATTCCGATCG	CTCCGGGAGC	TATCACCAGG	TACTCGGTTT	CGATGTTTTT	CCCGCGCCCT	68
TCCGTTGGCC	TGGGCCACCG	GTCTTTCAAT	GGGCTCTCTT	TGGGATTTGG	AATTTGAGAC	128
AACGAAATCG	GGCGATGGGT	GAGCAATCGT	CGCTGATGCA	AGACACGGCT	TGCTGGCGGC	188
CGCTTCAGGT	GGGATTTAAG	CCAGCGTATC	AACGTAGACC	GGCCACTGAG	CAGAACCCCA	248
ACCCACAAAC	CGTGGAGCGA	TGCGGCTCTC	GGGCGTCAAA	TTCCGGGTAG	ATATCGTATA	308
CCGATATCGG	ATTCGGTAGC	CTTATCGAGG	CATGAGAGCG	CCGCTAGACC	GACCGATAT	368
TCCAGATGAG	CTGCGGGCAC	CGCTGGGACT	CTTGAATGCG	GTGGTGATCG	GCTTGGGTC	428
CATGATCGGT	CCCGGAATCT	TTGCTGTTGG	CGAATTCGCG	ACGAGCTGCG	GGCGAATTCG	488
GCACGAGATG	CCAATCCCCA	GAAAGTCCGA	CAAGCCGTCA	ATGGCAGCTG	ATCGTTGGAT	548
CGATAGAGAA	CGCTCTGCTC	ATGCTTGCCG	CCTATCTCAA	CGGTGCTGGA	TTCCATGGAT	608
TAGCTTTGGT	TCTGCAATGC	ACGCTTAGAG	CCTACAGTCT	GGCTGTCTAT	CTTGGCCGAT	668
GTCAACAGTT	TTTTCATGTC	TAGCAGATCT	GTGAGTTTTC	AGTTGGTGAA	GACCGCATGT	728
TCACTTGTTC	TGACTACAT	CCTCTGCGCA	CATTTCGCTC	CCTGCAACTG	CGCTGCGACA	788
ATGGGCGAAC	CCCGGTGTAG	CTCGTGCGCA	ATTCGGCAGC	AGGATCCACC	GGAGATGGGC	848
GACGAGTACG	ACGAGGCGTC	GATGCTCAAC	ACCGTCTTTC	ACTATCACAA	CGGAGACGCA	908
AAAGAAAGAG	TGATCATCT	CGTCCCGCAG	GTGACAGAGG	AGAGGGCGCC	CATCGAATCT	968
GTAAACCAAG	TAGACAAAGG	GGGACATGAG	ACTGCTCTAC	GATGGGGGAG	CAGCTTTTCA	1028
TACAGAGAAC	ATCTTAGGTT	TTGATTCCGG	AACATCTTA			1058

(i) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

GCACGAGGCA TTGGGGGCA TCTGCATAAA CGGTGACGTA TCAGCAGAAA ACACCGGAGA	60
GAACAAACATG CGATCAGAAC GTCTCCGGTG GCTGGTAGGC GCAGAAAGGC CGTTCCGCTC	120
GGGTATTTGC GAGGACTTGC ACGACTCTTG CAG	153

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 387 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) SEQUENCE DESCRIPTION: SEQ ID NO:133:

CCCGCCGGTC GATCAGGAGG CAGGCGCAAA ACTCTGTCGA GCGGAGAGTC ATGATGTTCA	60
CCCGCGCGAG CATCTGGGGA ACGATCACCT CGATGTGCTT GTGCTGAAAT GACACACCTT	120
GGCGCGGATA GACTCTCTGG ACCTTGGGAA CAGGTGTAT CTGCACTCG CGGGGGGCTT	180
GCACCCGCAO CAGCTATGC GGGTGGGCGG AGCCTTCAT CAGCTGCTGG CCACCTCGA	240
CGTGGTGGCC ATCGGAGAGC ACCCGTTGG AACCTCTT GTGCTTGAC ACCCGAGCT	300
GCTGCGCTT GAGATCTTG TCTAGACCA CTTCCTCACC GCGCTGCTCA GGAACATGG	360
TGATCTTTTA GACCGGCTCG CGTCTCT	387

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 389 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) SEQUENCE DESCRIPTION: SEQ ID NO:134:

GTTGAGCAGC GCTATCGAT TGTGCGCTTC GCTTCGGTGG GTGCTGAACA CGGATCGAC	60
ATGCTGCTCG ACAAGCAATC CCCACTGCTG GCACCGGTCC AGTTCCTCGC CGAGAAGCTG	120
CTCGGCGGCA AAGACGGTCC GGGCTTGCTC CTTGGTGTGG GACTGACACC GGTACGCGCC	180
CCCAACGGCC AGTATTACTG GTTCGGCGAG CCAAGCGACA CCACAGAGTT TATGAGGCGC	240
CAAGTCGAGC ATAAAGCCGC ACGCAGGGTG CGCAGCGTG CGCGCGCGGC TATCGACAC	300
GGCATCGAGC TGATGCTGGC CGAGCGGCGA GCGGATCGAA ATCGATGCTT GGTGAGACGG	360
CTCTTCGCTT CGACGCGCTA AGCGCGCTC	389

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 460 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) SEQUENCE DESCRIPTION: SEQ ID NO:135:

CCGCGCGCTGG	GAATGATCCG	CCTCTGCTGG	CGCGCCCATG	TGATGCTGTT	GATGAGCTGT	60
TTGGAGAAGC	CCGGTTGGCG	TACCGGTGAG	CGGAATATC	TGTTGGAAGC	GTACCGGGAT	120
GTNCACATGA	ATTNCTNTGN	CCGCTGTCGG	CTNTTGTGCTG	GGGNAAACAC	GTGTCTGNTA	180
AGCCTTGNTG	GCTCTGGAAG	NGCGGTGAC	GCTTGTGTGG	CCGAGATAA	TGAGCAGCTG	240
ACGGTTGGGG	GGATCGCGCT	TATCCCAAGG	AATTCCGAGG	TGGTCCCGG	AGATGCCGAA	300
GCGTTCCAGG	GTCCTGTGCG	GCGTGTGCG	TCGGTCCAG	CACCTCCCGA	GGCATGTGCG	360
AGCCCGCGCG	AGCTTGGCAC	CAGGATTCGG	CGCGCGCGCG	GGAGCAGGCT	CGGNNCTGHN	420
NCGTGNTTCC	TNNNGCCAA	TNNACTCGN	CCNACAACT	TNNNCCGAC	TNNAGCCGN	480

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 587 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

GUAGCGGGCT	ACCGCGCGCT	CGCCGCGCAT	CGCCTGGATG	CAGCGCTAGC	CACCTGTNCA	60
TNCAGCGGGT	CGCGCGCGCG	GTCCGCGCTT	AACGCTATAG	CAGCTTCGAA	CGACCGAGCG	120
CGCGCATTA	CTTTGATGTT	GAACCGATGA	CCATGCGCTN	CGGTTGAAAT	CTGCTCTGTT	180
NGCGCGCGCG	TATTTNNGCG	ATAMATTGCG	TNNNAGCGCG	AAGCTAGAGC	GTATCGAGTT	240
CCCTTTTCAG	CACCGGCTCA	ATGTCAGCA	TCTTGTGGGG	AACATGAGCG	CGCGCGGACC	300
CGCGCGTTTC	CAATGTGTGA	GTTCAGAAAG	GTCTGACAAAG	CCAGCTGAAT	GTCTGCGGTA	360
GGGACGCGCG	GGCTGGGCTG	GGTGGGGTGA	CGCGCGCGCT	TCTGAAAGCG	AGGGGAGCCC	420
CGGACTCTTT	ACGCGCGGAG	CGCGCGCGGT	GTGCTGATG	TAGCGTGGCG	GGCAGTGGTT	480
GNTNACCCAA	CAGGATGAC	NACAAATAAN	CGGAGGAGAG	ACAGNGAGCG	GGCGGAGWAG	540
CTNACCGCGG	GTGNNNGCAA	NNNACGACAC	TNTACCGGNN	CTTATGNN		587

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1280 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

CAGGCGATGAG	CAGGCGCTTC	ATCATCGATC	CAAGGATCAG	TGCCATTGAC	GGCTTGTAGC	60
ACCTTCTGGG	GATTGGAATA	CCCAACCAAG	GGGATATCCT	TTACTCTCTA	CTAGATTAAT	120
TCGAARAAGC	CCTGGAAGAG	CTGGCAGCAG	CGTTTCTGGG	TGATGGCTGG	TGAGGTTCCG	180
CGCGGAGACA	ATACGCGGGC	AAAAACCGCA	ACGACGTGAA	TTTTTTCTAG	GAATGCGCAG	240
ACCTCGATGCG	TGAGTGCATC	AGCTTGATCC	ACGACGAGCG	CAAGCGGGTC	CAGACGAGCT	300
CGGACTGCTT	CGAGGCGCCC	TAGAAAGGTC	TGAGTTTCTT	CGCGCGGGTC	GCTGTGGAGC	360
TGAGCTAGAT	CGCGGTGCTC	GGGACAGCCC	TATCGGCGCG	CTTCCAGGCG	CGGTTTGTGG	420
CGGCGCGGAT	GGCGGTAGTG	GGGCGCGCGC	TTGGCTACTT	GCTCGTGAAA	ACGCTGATCA	480
ACGCGACTCA	ATCTCTGAAA	TTGCTTGCCA	AATTGGGCGA	GTGGGTGCGG	GGCGCATTTG	540
CGGAGCTCAT	TTGAGATGCG	CGGAGACTCA	TGAAGGCGAC	CTTGGGAGAA	GTGGGGGAGT	600

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TCATCACAAA CCGCTCAAC GGGTGAAG AGCTTTGGGA CAAGCTAAGG GGGTGGGTGA 660
CCGACTGTT CTCTGAGGG TGGTGAAGC TGGAGTGCTT CTTTGGGGG GTCCCCGGCT 720
TGACCCGGCG GAGCAGGGG TTTTGGCAAG TGACTGGCTT GTTCGGTGG GCGGCTCTGT 780
CGCATCGTC GGGTTTGGCT CAGCGGATA GCTTGGGAG CTCAGCCAGC TTGCTCGGCC 840
TGGCCCGCAT TGGGGGGGG TCGGTTTIS GGGCTTGGC GAGCTGGCT GAGTTCATG 900
CGGCTCAAC TGGGAGGCH CTACGGGCGG GAGCTGATG CCGGCTGGG GCGGTCGCG 960
AGCAGTGGG CGGGCACTG CAGCTGTCT CCGCGAGGG TTCCCAAGT ATGGGCGGAC 1020
CGGTAGCAT GGGGAGCAT CCCCCCTCT CGGGGGGCT GAAAGGAGC AGGAGAGGA 1080
AGTACTCGGA AGGACGGCG GCGGCACTG AGGACGGCG GCGGCGGCA GTGAGAGCT 1140
ACGGGGGGG TGGCAAAAG GTCTGTGTAC GAAACGTCT CTACCGCAT GCGGAGGCA 1200

```

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 392 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

```

Met Ser Arg Ala Phe Ile Ile Asp Pro Thr Ile Ser Ala Ile Asp Gly
1      5      10      15
Leu Tyr Asp Leu Leu Gly Ile Gly Ile Pro Asn Gln Gly Gly Ile Leu
20      25      30
Tyr Ser Ser Leu Glu Tyr Phe Glu Lys Ala Leu Glu Glu Leu Ala Ala
35      40      45
Ala Phe Pro Gly Asp Gly Trp Leu Gly Ser Ala Ala Asp Lys Tyr Ala
50      55      60
Gly Lys Asn Arg Asn His Val Asn Phe Phe Gln Glu Leu Ala Asp Leu
65      70      75      80
Asp Arg Gln Leu Ile Ser Leu Ile His Asp Gln Ala Asn Ala Val Gln
85      90      95
Thr Thr Arg Asp Ile Leu Glu Gly Ala Lys Lys Gly Leu Glu Phe Val
100     105     110
Arg Pro Val Ala Val Asp Leu Thr Tyr Ile Pro Val Val Gly His Ala
115     120     125
Leu Ser Ala Ala Phe Gln Ala Pro Phe Cys Ala Gly Ala Met Ala Val
130     135     140
Val Gly Gly Ala Leu Ala Tyr Leu Val Val Lys Thr Leu Ile Asn Ala
145     150     155     160
Thr Gln Leu Leu Lys Leu Leu Ala Lys Leu Ala Glu Leu Val Ala Ala
165     170     175
Ala Ile Ala Asp Ile Ile Ser Asp Val Ala Asp Ile Ile Lys Gly Thr
180     185     190
Leu Gly Glu Val Trp Glu Phe Ile Thr Asn Ala Leu Asn Gly Leu Tyr
195     200     205
Glu Leu Tyr Asp Lys Leu Thr Gly Trp Val Thr Gly Leu Phe Ser Arg
210     215     220
Gly Trp Ser Asn Leu Glu Ser Phe Phe Ala Gly Val Pro Gly Leu Thr
225     230     235     240
Gly Ala Thr Ser Gly Leu Ser Gln Val Thr Gly Leu Phe Gly Ala Ala
245     250     255

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Gly Leu Ser Ala Ser Ser Gly Leu Ala His Ala Asp Ser Leu Ala Ser
260 265 270
Ser Ala Ser Leu Pro Ala Leu Ala Gly Ile Gly Gly Ser Gly Phe
275 280 285
Gly Gly Leu Pro Ser Leu Ala Glu Val His Ala Ala Ser Thr Arg Gln
290 295 300
Ala Leu Arg Pro Arg Ala Asp Gly Pro Val Gly Ala Ala Gln Gln
305 310 315 320
Val Gly Gly Gln Ser Glu Leu Val Ser Ala Gln Gly Ser Gln Gly Met
325 330 335
Gly Gly Pro Val Gly Met Gly Gly Met His Pro Ser Ser Gly Ala Ser
340 345 350
Lys Gly Thr Thr Thr Lys Lys Tyr Ser Glu Gly Ala Ala Ala Gly Thr
355 360 365
Glu Asp Ala Glu Arg Ala Pro Val Glu Ala Asp Ala Gly Gly Gln
370 375 380
Lys Val Leu Val Arg Asp Val Val
385 390

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 439 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

ACGTTTACCC	ATGCGGTCGG	TGCAGAGCAA	CACAGAGCAA	CACAAATAG	TCTAATTCG	62
TTATAAGCCA	GACATTTCGG	TGCTATGATA	GAAGATGTC	ACCGATCAGA	TGAAGCGATC	120
CGCCTCAGGT	GGTATCCGAT	GTCTTTTGTG	ACCATACAGC	CGGTGCTCTT	GGCAGCGCGC	180
ACGGGGGAGT	TGCCGACGAT	CGGTACCGGC	GTGAGTGCTT	GGAAACACAG	CGTCTGTGCT	240
CGGACGAGCG	GGTATTACCC	CCCTGCTGCC	AATGACGTGT	CGGTCTGAG	GGCGGCGCGC	300
TTCAACGGCG	ACACCAAGCA	CTACGAGTGT	GTGAGTACG	CGGCGCGCTT	GGTCCATAGC	360
ATGTCTGTCG	CCCTCCGCG	GGCCACCGGC	GATCGGTATG	CGACACCGCA	GGCGCTCAAT	420
GTGTGCGGCA	CGGTTAAG					439

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1441 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

GAGGTGCTG	GCATGGATT	TGGGCTTTT	ACCTCCGAA	GTGAATTCAC	GCAGATGTA	60
TTCCTGTCG	GGGCGGAGT	CGAGCTAGC	CGCCGCGGC	GCCTGCGAGC	GTGTGCTGC	120
GGAGTCTACT	TGGCGCGCG	TCTGTATG	ATCGGTGCTG	TGACAGCTGA	TCTTTGAGC	180


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GTGGATGGGG  CGGCGCGGGG  CGGCGATGGC  GGGCGCGGCA  AGCGCGTATG  TGGCGTGGCT  240
GGCGCGCGAG  GGGCGCGTGG  CGAAGCGAGC  GGGCGCGAGC  CGGCGCGAGC  CGGCGCGAGC  300
GTTCGGGACC  GGGTTCGGGA  TGGCGGTGGC  AGCATCGCTC  GTGCGGGGCA  AGCGCGAGCG  360
GTTCGATGTC  CTGGTTCGGG  CGAAGCATTC  GGGCGGAAAC  AGTGGCGGCA  TGGCGGCTAC  420
CCAGCGCGAG  TATGGCGGAA  TGTGGCGGCA  AGAGCGTGGC  GTGATGTACA  GGTATGAGGG  480
GGCATCGGG  CGGCGGTGGG  GGTGGCGGCG  GTTCACTGCA  CGCGTGGGAG  GCGCGCGGCG  540
GGCGCGGGCG  GGGCGCGGAG  CGGCGCGGAG  CGAAGCGGCG  GGTGGCGGCG  CGTTCGGGCA  600
TGCACAGGCG  ACACTGGGCG  AGTGGCGGCG  GGGGATCGTG  AGCGACATTC  TGTGGCGATT  660
GGCGCGGAGC  GGTGATCGGG  TGCATCGGGG  AGTGTGGGGG  ATGCGGTGCA  CGCTGCAACCT  720
CGAAGTCGGA  TCGGCTGAGC  CGATGCTGAT  CGCGCGCGCG  ATAGGGGGAT  TGGAGCTGAT  780
CGCGCTCTAC  ATTGATGCGA  TCGCGAGCGG  GAGCATTCGG  CTGCGGATCA  CGAAGCGGCG  840
CAGACCTTGG  CACATCGGCG  TATACGGGAA  GCGCGCGGCG  CTGCGGATCA  CGAAGCGGCG  900
TGCATCGGAT  TGGCGGAGCG  AGGAGCGGAA  GCGCGGCTGG  GCGCGCTTGG  GGGCGCGGCG  960
CGCGGTGTCG  GGGCGGTCGG  GCGCGGAGCG  ATTAGTCGGA  GCGTGTGTCG  TGGCGGAGCG  1020
CTGGCGGAGC  GGGCGGCGCG  AGATCGGCTC  GCGCGTTCAG  GCGACAGCGA  CTTCGAGCTC  1080
CAGCGCTGGC  GCGCGGCGCG  CGGCGCTAAA  CGGCGGTCGG  GCGCGGCTGG  TCGCGGAGAT  1140
GGCTTTCGGC  AGCGTTCGGG  CAGCGGCGCG  GAGCGGCGGT  GCGCGGCGCG  GTAGCGGCGC  1200
CAGCATGAGC  GCGCGGAGCG  AGCGCGGCGA  AGCGCGGCGT  GTTGTGATTA  GAGCGGAGCG  1260
CGCGCGGCGA  AGCGCGGCGG  GGTAAAGATC  CGCGACCGCT  TGTGTGCGCG  CGCGGAAATG  1320
CGTGTGAGCT  CTGCGTATCG  GAGCGGCGGT  TACACCGGCT  TGTGTGAGCG  TACGCGTATG  1380
CAGCGGCGGT  TGTGATTCCT  GCGCGGCTAT  CAGAGCGGAT  TGTGTGCGAA  CCGCGGAGAA  1440
G

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(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:

- (a) LENGTH: 99 amino acids
- (b) TYPE: amino acid
- (c) STRANDEDNESS: single
- (d) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

```

Met Ser Phe Val Thr Ile Gln Pro Val Val Leu Ala Ala Ala Thr Gly
 1          5          10          15
Asp Leu Pro Thr Ile Gly Thr Ala Val Ser Ala Arg Asn Thr Ala Val
 20          25          30
Cys Ala Pro Thr Thr Gly Val Leu Pro Pro Ala Ala Asn Asp Val Ser
 35          40          45
Val Leu Thr Ala Ala Arg Phe Thr Ala His Thr Lys His Tyr Arg Val
 50          55          60
Val Ser Lys Pro Ala Ala Leu Val His Gly Met Phe Val Ala Leu Pro
 65          70          75          80
Ala Ala Thr Ala Asp Ala Tyr Ala Thr Thr Glu Ala Val Asn Val Val
 85          90          95
Ala Thr Gly

```

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

- (a) LENGTH: 423 amino acids
- (b) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

```

Met Asp Phe Gly Leu Leu Pro Pro Gln Val Asn Ser Ser Arg Met Tyr
 1          5          10          15
Ser Gly Pro Gly Pro Glu Ser Met Leu Ala Ala Ala Ala Trp Asp
 20          25          30
Gly Val Ala Ala Glu Leu Thr Ser Ala Ala Val Ser Tyr Gly Ser Val
 35          40          45
Val Ser Thr Leu Ile Val Gln Pro Trp Met Gly Pro Ala Ala Ala Ala
 50          55          60
Met Ala Ala Ala Ala Thr Pro Tyr Val Gly Trp Leu Ala Ala Thr Ala
 65          70          75          80
Ala Leu Ala Lys Glu Thr Ala Thr Gln Ala Arg Ala Ala Ala Gln Ala
 85          90          95
Phe Gly Thr Ala Phe Ala Met Thr Val Pro Pro Ser Leu Val Ala Ala
100          105          110
Asn Arg Ser Arg Leu Met Ser Leu Val Ala Ala Asn Ile Leu Gly Gln
115          120          125
Asn Ser Ala Ala Ile Ala Ala Thr Gln Ala Glu Tyr Ala Glu Met Trp
130          135          140
Ala Gln Asp Ala Ala Val Met Tyr Ser Tyr Glu Gly Ala Ser Ala Ala
145          150          155          160
Ala Ser Ala Leu Pro Pro Phe Thr Pro Pro Val Gln Gly Thr Gly Pro
165          170          175
Ala Gly Pro Ala Ala Ala Ala Ala Thr Gln Ala Ala Gly Ala Gly
180          185          190
Ala Val Ala Asp Ala Gln Ala Thr Leu Ala Gln Leu Pro Pro Gly Ile
195          200          205
Leu Ser Asp Ile Leu Ser Ala Leu Ala Ala Asn Ala Asp Pro Leu Thr
210          215          220
Ser Gly Leu Leu Gly Ile Ala Ser Thr Leu Asn Pro Gln Val Gly Ser
225          230          235          240
Ala Gln Pro Ile Val Ile Pro Thr Pro Ile Gly Glu Leu Asp Val Ile
245          250          255
Ala Leu Tyr Ile Ala Ser Ile Ala Thr Gly Ser Ile Ala Leu Ala Ile
260          265          270
Thr Asn Thr Ala Arg Pro Trp His Ile Gly Leu Tyr Gly Asn Ala Gly
275          280          285
Gly Leu Gly Pro Thr Gln Gly His Pro Leu Ser Ser Ala Thr Asp Glu
290          295          300
Pro Glu Pro His Trp Gly Pro Phe Gly Gly Ala Ala Pro Val Ser Ala
305          310          315          320
Gly Val Gly His Ala Ala Leu Val Gly Ala Leu Ser Val Pro His Ser
325          330          335
Trp Thr Thr Ala Ala Pro Gln Ile Gln Leu Ala Val Gln Ala Thr Pro
340          345          350
Thr Phe Ser Ser Ser Ala Gly Ala Asp Pro Thr Ala Leu Asn Gly Met
355          360          365
Pro Ala Gly Leu Leu Ser Gly Met Ala Leu Ala Ser Leu Ala Ala Arg
370          375          380

```

Gly Thr Thr Gly Gly Gly Gly Thr Arg Ser Gly Thr Ser Thr Asp Gly
 185 190 395 400
 Gln Glu Asp Gly Arg Lys Pro Pro Val Val Val Ile Arg Glu Gln Pro
 405 410 415
 Pro Pro Gly Asn Pro Pro Arg
 420

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

Met Ser Leu Leu Asp Ala His Ile Pro Gln Leu Val Ala Ser Gln Ser
 1 5 10 15
 Ala Phe Ala Ala Lys Ala Gly Leu Met Arg His Thr Ile Gly Gln Ala
 20 25 30
 Glu Gln Ala Ala Met Ser Ala Gln Ala Phe His Gln Gly Glu Ser Ser
 35 40 45
 Ala Ala Phe Gln Ala Ala His Ala Arg Phe Val Ala Ala Ala Lys
 50 55 60
 Val Asn Thr Leu Leu Asp Val Ala Gln Ala Asn Leu Gly Glu Ala Ala
 65 70 75 80
 Gly Thr Tyr Val Ala Ala Asp Ala Ala Ala Ala Ser Thr Tyr Thr Gly
 85 90 95
 Phe

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

Cys Arg Leu Cys Leu Asp Ser His Leu Arg Val Val Ala Leu Pro Ala
 1 5 10 15
 Gly Gln Pro Gly Arg Leu Val Gln Ala Ile Gly Pro Ala Gln Gln Arg
 20 25 30
 Asp Val Gly Gln Thr Arg Cys Thr Arg Thr Gly Leu Asp Xaa Val Ser
 35 40 45
 Ala Leu Thr Ala Ala Gln Phe Ala Ala His Ala Gln Ile Tyr Gln Ala
 50 55 60
 Val Ser Ala Gln Ala Ala Ala Ile His Glu Met Phe Val Asn Thr Leu

92

Gln Asn Xaa Ser Gly Ser Tyr Ala Ala Thr Glu Ala Ala Asn Ala Ala
85 90 95

Ala Ala Gly

Claims

1. A polypeptide comprising an immunogenic portion of a *M. tuberculosis* antigen, or a variant of said antigen that differs only in conservative substitutions and/or modifications, wherein said antigen comprises an amino acid sequence encoded by a DNA sequence selected from the group consisting of the sequences recited in SEQ ID NO: 1, 11, 12, 83, 103-108, 125, 127, 129-137, 139 and 140, the complements of said sequences, and DNA sequences that hybridize to a sequence recited in SEQ ID NO: 1, 11, 12, 83, 103-108, 125, 127, 129-137, 139 and 140, or a complement thereof under moderately stringent conditions.
2. A polypeptide comprising an immunogenic portion of a *M. tuberculosis* antigen, or a variant of said antigen that differs only in conservative substitutions and/or modifications, wherein said antigen comprises an amino acid sequence selected from the group consisting of sequences recited in SEQ ID NO: 16-33, 109, 126, 138, 141, 142 and variants thereof.
3. A DNA molecule comprising a nucleotide sequence encoding a polypeptide according to any one of claims 1 and 2.
4. An expression vector comprising a DNA molecule according to claim 3.
5. A host cell transformed with an expression vector according to claim 4.
6. The host cell of claim 5 wherein the host cell is selected from the group consisting of *E. coli*, yeast and mammalian cells.
7. A pharmaceutical composition comprising at least one polypeptide according to any one of claims 1 and 2 and a physiologically acceptable carrier.

8. A pharmaceutical composition comprising at least one DNA molecule according to claim 3 and a physiologically acceptable carrier.

9. A pharmaceutical composition comprising at least one DNA molecule having a sequence recited in SEQ ID NO: 2-10, 102, 128, and a physiologically acceptable carrier.

10. A vaccine comprising at least one polypeptides according to any one of claims 1 and 2 and a non-specific immune response enhancer.

11. A vaccine comprising:
at least one polypeptide encoded by a DNA sequence selected from the group consisting of SEQ ID NO: 2-10, 102, 128, the complements of said sequences, and DNA sequences that hybridize to a sequence recited in SEQ ID NO: 2-10, 102, 128; and
a non-specific immune response enhancer.

12. The vaccine of claims 10-11 wherein the non-specific immune response enhancer is an adjuvant.

13. A vaccine comprising at least one DNA molecules according to claim 3 and a non-specific immune response enhancer.

14. A vaccine comprising at least one DNA molecule having a sequence recited in SEQ ID NO: 2-10, 102, 128; and a non-specific immune response enhancer.

15. The vaccine of claims 13 or 14 wherein the non-specific immune response enhancer is an adjuvant.

16. A method for inducing protective immunity in a patient, comprising administering to a patient a pharmaceutical composition according to any one of claims 7-9.

17. A method for inducing protective immunity in a patient, comprising administering to a patient a vaccine according to any one of claims 10-13.

18. A fusion protein comprising at least two polypeptides according to any one of claims 1 and 2.

19. A fusion protein comprising a polypeptide according to any one of claims 1 and 2 and a known *M. tuberculosis* antigen.

20. A pharmaceutical composition comprising a fusion protein according to any one of claims 18 and 19, and a physiologically acceptable carrier.

21. A vaccine comprising a fusion protein according to any one of claims 18 and 19, and a non-specific immune response enhancer.

22. The vaccine of claim 21 wherein the non-specific immune response enhancer is an adjuvant.

23. A method for inducing protective immunity in a patient, comprising administering to a patient a pharmaceutical composition according to claim 20.

24. A method for inducing protective immunity in a patient, comprising administering to a patient a vaccine according to any one of claims 21 and 22.

25. A method for detecting tuberculosis in a patient, comprising:

(a) contacting dermal cells of a patient with at least one polypeptide according to any one of claims 1 and 2; and

(b) detecting an immune response on the patient's skin and therefrom detecting tuberculosis in the patient.

26. A method for detecting tuberculosis in a patient, comprising:
- (a) contacting dermal cells of a patient with at least one polypeptide encoded by a DNA sequence selected from the group consisting of SEQ ID NO:2-10, 102, 128, the complements of said sequences, and DNA sequences that hybridize to a sequence recited in SEQ ID NO:2-10, 102, 128; and
 - (b) detecting an immune response on the patient's skin and therefrom detecting tuberculosis in the patient.
27. The method of any one of claims 25 and 26 wherein the immune response is induration.
28. A diagnostic kit comprising:
- (a) a polypeptide according to any one of claims 1 and 2; and
 - (b) apparatus sufficient to contact said polypeptide with the dermal cells of a patient.
29. A diagnostic kit comprising:
- (a) a polypeptide encoded by a DNA sequence selected from the group consisting of SEQ ID NO: 2-10, 102, 128, the complements of said sequences, and DNA sequences that hybridize to a sequence recited in SEQ ID NO: 2-10, 102, 128; and
 - (b) apparatus sufficient to contact said polypeptide with the dermal cells of a patient.

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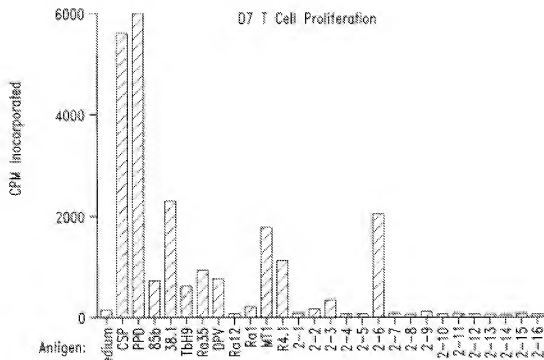


Fig. 1A

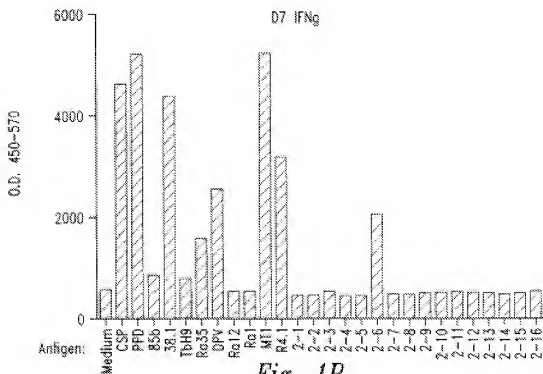


Fig. 1B

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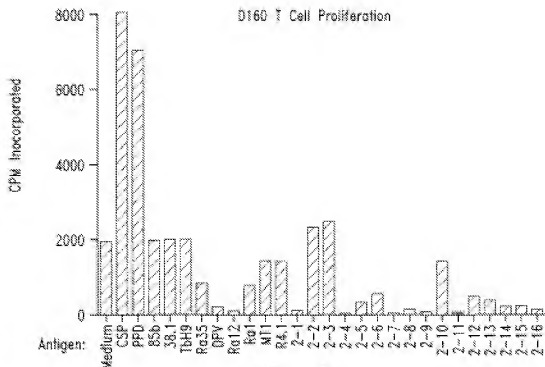


Fig. 2A

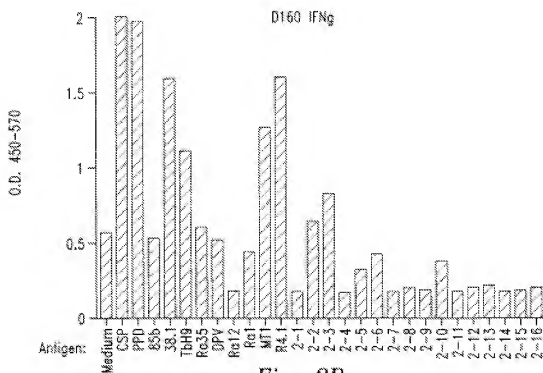


Fig. 2B